

2 32
 CTT TCA GAA GCC CGG GAG AGC GTC TTG GGG GAT TTG CTG AAG GTT GTG CTG TAC AGC CTG
 leu ser glu ala arg glu ser val leu gly asp leu leu lys val val leu tyr ser leu
 62 92
 GCG AGT GCC CAG AGT GCC CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG AGG GCC CTT GTG
 gly ser ala gln ser ala leu phe leu gln his gly leu ala thr gln arg ala leu val
 122 152
 TCC AAG TTC CCG GAG CTG CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC GAC CTG TGC CTG
 ser lys phe pro glu leu leu phe glu glu asp thr glu leu cys ala asp leu cys leu
 182 212
 AGC CTT CTA CGA CAC TGT GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC GCC AGC GCC TCG
 arg leu leu arg his cys gly ser arg ile ser thr ile arg thr his ala ser ala ser
 242 272
 CTG TAC CTG CTC ATG CGA CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC CGT GTG AAG ATG
 leu tyr leu leu met arg gln asn phe glu ile gly his asn phe ala arg val lys met
 302 332
 CAG GTC ACC ATG TCT CTC TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC AGT GAA GAG CAC
 gln val thr met ser leu ser ser leu val gly thr thr gln asn phe ser glu glu his
 362 392
 CTG CGA CGT TCA CTC AAA ACC ATC CTC ACC TAT TGT GAG GAG GAC ATG GGG CTG CGG GAC
 leu arg arg ser leu lys thr ile leu thr tyr ala glu glu asp met gly leu arg asp
 422 452
 AGC ACC TTC GCA GAG CAG GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG ATC CTG ACG GAC
 ser thr phe ala glu gln val gln asp leu met phe asn leu his met ile leu thr asp
 482 512
 ACG GTG AAG ATG AAG GAA CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC CTC ATG TAC AGA
 thr val lys met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg
 542 572
 ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG CAG AAC ATG GCC
 ile ala arg gly tyr gln gly ser asp leu arg leu thr trp leu gln asn met ala
 602
 GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG GTG CAC GCG GCC
 gly lys his ala glu leu gly asp his ala glu ala ala gln cys met val his ala ala
 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
 692
 GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAC GGC CAC CTG CCC GTG GGC TGC
 ala leu val ala ala glu tyr leu ala leu leu glu asp his arg his leu pro val gly cys
 722 752
 GTT TCC TTC CAG AAC ATC TCA TCC AAT GTG CTA GAG GAG TCC GCC ATC TCC GAC GAC ATC
 val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile ser asp asp ile
 782 812
 CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG CTG GGG CTG GTA
 leu ser pro asp glu gly gly phe cys ser gly lys his phe thr leu leu gly leu val
 842 872
 GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC GAG GCG GTG AAT
 gly leu leu glu gln ala ala gly phe thr met gly gly leu tyr glu gln ala val ala
 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

FIG. 1 (1 of 3)

902 932
GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC AAG AAG CTG GCC
glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr lys lys leu ala

962 992
CGG GTG CAC GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG AGT TCC GGC TGG
ala val his gly lys leu gln glu ala phe thr lys ile met his gln ser ser gly trp

1022 'xxxxx ITAM xxxxx|1052
GAG CGC GTG TTC GGG ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC TTC GGT GAC CTG
glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his phe gly asp leu

1082 1112
GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA GAG ATC TCA CAC
asp glu gln glu phe val tyr lys glu pro ser ile thr lys leu ala glu ile ser his

1142 1172
CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG ATT ATC AAA GAC
arg leu glu glu phe tyr thr glu arg phe gly asp asp val val glu ile ile lys asp

1202 1232
TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC CAG ATC ACG TAT
ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile gln ile thr tyr

1262 1292
GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC TTT GAC CGC AAC
val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr phe asp arg asn

1322 1352
TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CGG GAT GGG CGC GCA CAC GGG
tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly arg ala his gly

1382 1412
GAG CTG CCC GAG CAA CAC AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC GCC TTC CCC TAC
glu leu pro glu gln his lys arg lys thr leu leu ser thr asp his ala phe pro tyr

1442 1472 |xxxxxxxxxxxx
ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG CCA GTG GAG GTG
ile lys thr arg ile arg val cys his arg glu glu thr val leu thr pro val glu val

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC GAG CAG GAC CCA
ala ile glu asp met gln lys lys thr arg glu leu ala phe ala thr glu gln asp pro

xx
CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC ACC GTG AAC CAG
pro asp ala lys met leu gln met val leu gln gly ser val gly pro thr val asn gln

1622 1652
GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC CCC AAG CTC TTC
gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp pro lys leu phe

1682 1712
CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA TGT GAG GAT GCG
arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys cys glu asp ala

|xx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC CGT GAG CTG GAG
leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his arg glu leu glu

FIG. 1 (2 of 3)

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XXX|
 CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG CGC CTG CCC CAG
 arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln arg leu pro gln

1862 1892
 CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA AGT TTC CGA AAG
 leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala ser phe arg lys

1922 1952
 GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG CAC CCG GGC CTC
 ala asp leu STP

1982 2012
 AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT GGG GTG ACC ACA

2042 2072
 CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA CTG ATG CTT CCT

2102 2132
 CCC TTT TTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

FIG. 1 (3 of 3)

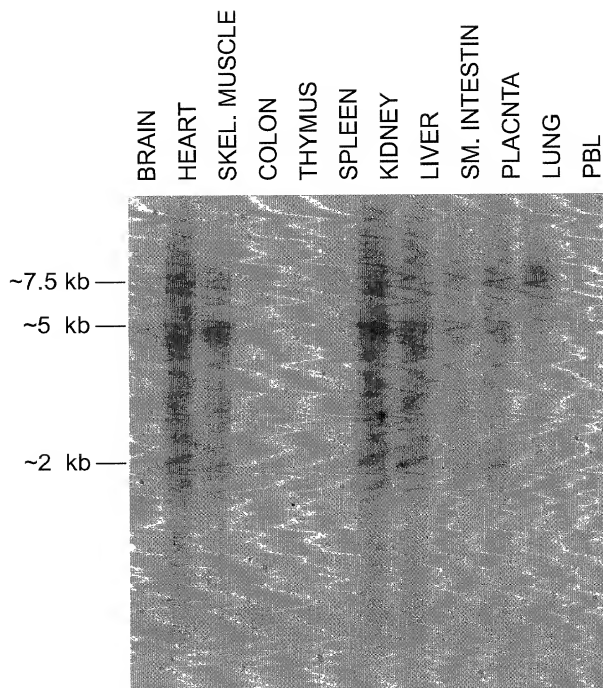


FIG. 2

HC2A -----
 KIAA ASGNLDKNARFSAIYRQDSNKLSDMDMLKLLADFRKPERMAKLPVILGNLDITIDNVSSD
 rat -----
 HC4 -----
 HC1 -----
 HC3 -----
 HC5 -----

HC2A -----
 KIAA FPNYVNSSYIPTKQFETCSKTPITEFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ
 rat -----
 HC4 -----
 HC1 -----
 HC3 -----
 HC5 -----

HC2A -----VLHHQNPPEFYDEIK
 KIAA KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGPVETRSAPAAVLHHQNPPEFYDEIK
 rat -----
 HC4 -----
 HC1 -----
 HC3 -----
 HC5 -----

HC2A IELPTQLHEKHHLLLTFFHVSCDNSSKSGSTKKRDVVETQVGYSWLPLKDGGRVVTSEQHI
 KIAA IELPTQLHEKHHLLLTFFHVSCDNSSKSGSTKKRDVVETQVGYSWLPLKDGGRVVTSEQHI
 rat -----
 HC4 -----
 HC1 -----
 HC3 -----
 HC5 -----

HC2A PVSANLPSGYLGQELGMRHYGPEIKWVDGKPLKISTHLVSTVYTQDQHLNFFQYC
 KIAA PVSANLPSGYLGQELGMRHYGPEIKWVDGKPLKISTHLVSTVYTQDQHLNFFQYC
 rat -----
 HC4 -----
 HC1 -----
 HC3 -----GPGPARSTVSIISLISNSARV
 HC5 -----

HC2A QKTESGAQALGNELVKYKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
 KIAA QKTESGAQALGNELVKYKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
 rat -----
 HC4 -----MEIQVLIREFLSVILMQLFWVLPMNIHEDDVPISCPMV
 HC1 -----MSFLPIILNQLFRVLV-QNEEDEITTTVTRV
 HC3 NRSRSLSNSNPDISGTPTSPDDEVRSIIGSGKGLDRSNSWNTGGPKAAPWGSNPSPSAES
 HC5 -----

FIG. 3A (1 of 5)

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HC2A I I H V V A Q C H E E G L E S H L R S Y V K Y A K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N
 KIAA I I H V V A Q C H E E G L E S H L R S Y V K Y A K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N
 rat -----
 HC4 L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K S A P A Q P L I H E T L A T M M I A L L K Q S A D F L A I N
 HC1 L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R --- A C K E R P V H E D L A K N V T G L L K --- S N D S P T V K
 HC3 T Q A M D R S C N R M S S H T E T S S F L Q T L T G R L P --- T K K L F H E E L A L Q V W V C S G --- S V R --- E
 HC5 -----

Cadherin
 Cleavage

HC2A K L L R Y S W F F F D V L I K S M A Q H L I E N S K V L I R N O R F P A S Y H H A E T V V N M L M P H I T Q K F G D
 KIAA K L L K Y S W F F F D V L I K S M A Q H L I E N S K V L I R N O R F P A S Y H H A V E T V V N M L M P H I T Q K F R D
 rat -----
 HC4 K L L K Y S W F F F E I I A K S M A T Y L L E E N K I K L T H G O R F P K A Y H H A L H S L F L A I T - I V E S Q Y A E
 HC1 H V L K H S W F F F A I I L K S M A Q H L I D T N K I Q L E R P Q R F P E S Y Q N E L D N L V M V L S D H V I W K Y D
 HC3 S A L Q Q A W F F F E L M V K S M V H H L Y F N D K L E A R K R S F P E R F E M D D I A A L V S T I A S D I V S R F O R
 HC5 -----

HC2A N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S --- C F A G D P K T L F E Y K F E L
 KIAA N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S --- C F A G D P K T L F E Y K F E L
 rat -----
 HC4 I P K E S R N V N Y S L A S F L K C C L T L M D R G F V E N L I N --- D Y I S --- G F S P K D P K V L A E Y K F E L
 HC1 A L E E T R A T H S V A R F L K R C F T F M D R G C V F K M V N --- N Y I S --- M F S S G D L K T L C Q K F D F L
 HC3 D T E M V E R L N T S L A F F L N D L L S V M D R G F V F S L I K S C Y K Q V S S K L Y S L P N P S V L V S L R L D F L
 HC5 -----

HC2A R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F
 KIAA R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F
 rat -----
 HC4 Q T I C N H E H Y I P L N L P M --- A F A K P K L O R --- V Q D S N L --- E Y S L S D E Y
 HC1 Q E V C Q H E H F I P C L P I R S A N I P D P T P S E S --- T Q E L H A S D M P E Y S V T N E F
 HC3 R I T C S H E H Y I T I N L P C S L L T P P A S P S P V S S A T S Q S S G F T N V Q D K I A N M F E L S --- V P F
 HC5 ----- M N A D T A P T S P C P S I S --- S Q N S S S C S S F D Q K I A S M F D R T S R V P A

Cadherin
 EC motif

HC2A C R N H F L V G I L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 KIAA C R N H F L V G I L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 rat -----
 HC4 C K H H F L V G I L L R E T S I A L Q D M Y E --- I R Y T A I S V I K N L L I K H A F D T R Y Q H K N Q Q A K I A Q
 HC1 C R K H F L G I L L R E V G F A L Q E D Q D --- V R H L A L A V L K N L M A K H S F D D R Y E P R K Q A Q I A S
 HC3 Q R Q H Y L A G I V T E L A V I L D P D A E G L F G L H K K V I N M V N L L S S H S D P R Y S D P Q I K A R V A M
 HC5 S S T S - S P G I L F T E L A A L D A E G E G I S E V O R K A V S A I H S L L S S H D L D P R C V K P E V K V I A A

HC2A L Y L P L F G L L I E N V Q R I N V R D V S ? F P V N A G - M T V K D E S L A P A V N P L V T P Q K G S T L D N S L H
 KIAA L Y L P L F G L L I E N V Q R I N V R D V S ? F P V N A G - M T V K D E S L A P A V N P L V T P Q K G S T L D N S L H
 rat -----
 HC4 L Y L P F V G L L E N I Q R L A G R D T L Y S C A A M P N S A S R D E F P C G --- F T S P --- A N --- R G S L S
 HC1 L Y M P L Y G M L D N M P R I Y L K D L Y P F T V N T S N Q G S R D D L S T N G G F Q S Q T A I K H A N S V D T S F S
 HC3 L Y L P L I G I I M E T V P Q L Y D F T E T H N Q R G R P I C I A T D D Y E S E --- S G --- S M T S
 HC5 L Y L P L V G I I L D A L P Q L C D F T V A D T R R Y --- T S G S D E Q E --- G A --- G A I T

FIG. 3A (2 of 5)

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HHC2A	KDLLGAISGLASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNLKDHHQSS
KIAA	KDLLGAISGLASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNLKDHHQSS
rat	-----
HC4	TDKDTAYGSFQNG-----HGIKREDSRGSLLIP-EGATGFPDQNGTGEN-----TRGS
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDNSFPSTNEKSEKTDNCKEIPPL
HC3	QTVAMATAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----
HC5	QNVALATAGNFFN-----LKTSG-IVLSSLPYRQYN-----
HC2A	TLGNSVVRCDKLDQSEIKSLMCFYLKLSMSDDALFTYWN-KASTSELMDFFTISEVCL
KIAA	TLGNSVVRCDKLDQSEIKSLMCFYLKLSMSDDALFTYWN-KASTSELMDFFTISEVCL
rat	-----
HC4	STRSSVSQYNRLDQYEIRSLMCFYLKLSMSDDALFTYWN-KVSPQELINILILLEVCL
HC1	ALIGSTLRFDRLDQAESTRSLMCFLHIMKTSYETLIAYWQ-RAPSPVSDFFSILDVCL
HC3	-----TFSAESSRSLICLLWLKMN-ADETVLQKWFTDLISVLQNRLLDLYLVCL
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLFLICV
HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
KIAA	HQFQYMGKRYIAR-----TGMM-----
rat	-----
HC4	FHFRYMGKRNRIARVHDRAWLSKHFGIDRKS-----QTFMFLNRNRSGVM
HC1	QNFYRLGKRNIIRKIAAAF--KFVQSTQNNGTLLKGSNPSCQTSGLLAQWHSSTRHEGKH
HC3	SCFEYKGKVVFERMNSLTFK--KSKDMRAK-----LEEALIGSARQEMV
HC5	LCFEYKGKQSSDKVSTQVLQ--KSDVKAR-----LEEALLREGARGSEHM
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIPHQALLEGNTATEVS
HC1	QHRSSQTLPIIRGK---NALSNPKL---LQMLDNTMTSNSNEIDIVHHVDTFANATEGC
HC3	RRSRGQLRSPSGSAFQSGENLWRKMDTFRQNTKEIKDRSARIEHEALIDGNLATEAN
HC5	RRRAPGNDRRFP----GLNEMLRWKKEQTHWRQANEKLDKTKAELDQEAALISGNLATEAH
HC2A	LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDDVYLCFLQKHQSEETALKNVFTALRSLIY
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDDVYLCFLQKHQSEETALKNVFTALRSLIY
rat	-----KLRSRGHSPMLKKVFDDVYLCFLQKHQSEEMALKNVFTALRSLIY
HC4	LTVLDTISFFTQCFKTHFINNDGHNPMLKKVFDDVYLCFLQKHQSEVSLKHVFASLRAFIS
HC1	LITLDLSLFTQTHQRLQCCDCQNSLMKRGFDTYMLFFQVQNSATLKHVFASLRLFCV
HC3	LITLDLTLIVVQTVS--VTES--KESILGGVLKVLLESMACNSAVYLOHCFCATQALVS
HC5	LIIIDMQENIIQASS--ALDC--KDSLLGGVLRVVLNSLNCQSTTYLTHCFATRALIA
HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSISIRTEASQLLYFLMRNNFDYTGKKSFVRTH
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSISIRTEASQLLYFLMRNNFDYTGKKSFVRTH
rat	KFPSTFYEGRADMCASLCYEVLLKCCNSKLSISIRTEASQLLYFLMRNNFDYTGKKSFVRTH
HC4	KFPSAFFKGRVNMCAAPCYEVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1	KFPSAFFQGPADLCGSPCYEVLKCCNHRSSRTQTAEALLYLLMRNNFEYTKRKTFLRTH
HC3	KFPPELLFEETEQCADLCRLRLRHCCSSSIGTIRSHPSASLYLLMRNNFEYTKRKTFLRTH
HC5	KFGPELLFEEEVEQCADLCRQVLLHCCSSSMVDVTRSQACATLYLLMRFSFGATS--NFAVRK
HC2A	LQVIIISVSQLIADVVIGGETRFQQSLSIINNCCANSRLIKHTSPSSDVKDLTKRIRTVLM
KIAA	LQVIIISVSQLIADVVIGGETRFQQSLSIINNCCANSRLIKHTSPSSDVKDLTKRIRTVLM
rat	LQVIIISVSQLIADVVIGGETRFQQSLSIINNCCANSRLIKHTSPSSDVKDLTKRIRTVLM
HC4	LQIIIAVSQLIADVALSGGSRFQESLPIINNCCANSRDLMLARAPAEVKDLTKRIRTVLM
HC1	LQIKAVSQLIAD-AGIGGSRFQHSIAITNNFANGDKQMKNSNPFPAEVDLTKRIRTVLM
HC3	MQVPMSSSLVGTSGNFNEEFLRRSLKTLITYAEDELERETTFPDQGVQLVFNHMLIS
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTTFFQVEELCNLSILY

FIG. 3A (3 of 5)

	Transmembrane
HC2A	ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKKTWLD SMARI HVKNGUL SEAAACVYVHV
KIAA	ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKKTWLD SMARI HVKNGUL SEAAACVYVHV
rat	ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKKTWLD SMARI HVKNGUL SEAAACVYVHV
HC4	ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKKTWLD SMARI HVKNGUL SEAAACVYVHV
HC1	ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKKTWLD SMARI HVKNGUL SEAAACVYVHV
HC3	DTVMKEHQEDPEMLIDLMYRIAKGYQTSPLRLTLWLQNMAGKHSERSNHAEAGCLVHS
HC5	DTVMKEHQEDPEMLIDLMYRIAKGYQTSPLRLTLWLQNMAGKHSERSNHAEAGCLVHS
	SH3
HC2A	TALVAEYLTRKGV-----FRQCTAPFRVITPN
KIAA	TALVAEYLTRKEA-----VQWEPPLPHSHSACLRRSGGVFRQCTAPFRVITPN
rat	TALVAEYLTRKEAD-----LALQREPPVPPYHSITSCQRKSRGGMFRQCTAPFRVITPN
HC4	AALVAEYLTRKKL-----FNGCSAFKKITPN
HC1	AALIAEYLTRKGYKVKVEKICTASLLSEDPHPCDSNSLLTTPSGGSMFSGMGWPAFLSITPN
HC3	AALVAEYLSMLE-----RKYLPGVCVTFQNISSN
HC5	AALVAEYLSMLE-----HSYLPVGSVSFQNISSN
	ITAM
HC2A	IDEEASVMEVDVGMQD-----VHFNEVDVLMELLEQCADGLNKAELVYELIADIYKLIPI
KIAA	IDEEASVMEVDVGMQD-----VHFNEVDVLMELLEQCADGLNKAELVYELIADIYKLIPI
rat	IDEEASVMEVDVGMQD-----VHFNEVDVLMELLEQCADGLNKAELVYELIADIYKLIPI
HC4	IDEEGAKKEDAGMMD-----VHYSEEVLELLEQCADGLNKAELVYELIADIYKLIPI
HC1	IKEEGAKKEDSGMMD-----TPYENILVEQLYMCGEFLNKAELVYELIADIYKLIPI
HC3	VLEESVSDSDVVSDEEGICSGRYTESGLVGLLEQAASFSMAGMYEAVNEVYKLIPI
HC5	VLEESVSDSDVVSDEEGICSGRYTESGLVGLLEQAASFSMAGMYEAVNEVYKLIPI
	ITAM ITAM ITAM ITAM
HC2A	YEKRRD-----YKRRDPERLAHLVDTLHRAYSKVTEVMHSGRRLLGTFRVAFPFQQAQYQFTDSETDVE
KIAA	YEKRRDPERLAHLVDTLHRAYSKVTEVMHSGRRLLGTFRVAFPFQQAQYQFTDSETDVE
rat	SMKSGGTLETHLVDTLHRAYSKVTEVITR-----A-----AGSWDLLPGGLFGQ
HC4	YENRRREFENLTQVRLTHGAYTKILEVMHTKKRLLG-----TFPRVAFYQG
HC1	FEKQRDPFKKLSIDVYDIHRSYLVKAEVNVSEKRLFG-----RFRVAFYQG
HC3	HEANRDAKKLSITHGKLEAFSKIVHQSTGWERMFG-----TFPRVAFYQG
HC5	LEAHRDFRKLTLTHSKLQAFDSIVNKDH-----KRMFG-----TFPRVAFYQG
	ITAM ITAM
HC2A	-FFFEDEGKHYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFA
KIAA	GFEEDEGKHYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFA
rat	GFEEDEGKHYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFA
HC4	SFFEDEGKHYIYKEPKLTGLSEISQRLKLYADKFGADNVKIQDSGKVNPKDLDSKFA
HC1	GFEEDEGKHYIYKEPKLTGLSEISQRLKLYADKFGADNVKIQDSGKVNPKDLDSKFA
HC3	TKFGDLEQHFVYKEPAITKLAEISHRLEAGYGEFGEDVVEVVKDSNVKPKDLDPNKA
HC5	SKFGDLEQHFVYKEPAITKLAEISHRLEAGYGEFGEDVVEVVKDSNVKPKDLDPNKA
	ITAM
HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMEFPPTQTGKRQGGVEEQCKRRITLTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMEFPPTQTGKRQGGVEEQCKRRITLTA
rat	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMEFPPTQTGKRQGGVEEQCKRRITLTA
HC4	YIQVTVVKPYFDOKELTERKTEFERNHNSRFEAPYPTLSGKKQGCIEQCKRRITLTT
HC1	YIQVTVVKPYFDOKELTERKTEFERNHNSRFEAPYPTLSGKKQGCIEQCKRRITLTT
HC3	YIQVTVVKPYFDOKELTERKTEFERNHNSRFEAPYPTLSGKKQGCIEQCKRRITLTT
HC5	YIQVTVVKPYFDOKELTERKTEFERNHNSRFEAPYPTLSGKKQGCIEQCKRRITLTT

FIG. 3A (4 of 5)

Coiled-Coil 1

HC2A	IHCFFPYVKKRIPVMYQHHTDLN	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLG	SV
KIAA	IHCFFPYVKKRIPVMYQHHTDLN	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLG	SV
rat	IHCFFPYVKKRIPVMYQHHTDLN	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLG	SV
HC4	SNSFFPYVKKRIPINCEQQINLK	IDGATDEIKDKTAELQLKCSSTDVMQIKLQLKLG	SV
HC1	SHLFFPYVKKRIVISQSSSTELN	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLG	SV
HC3	SHAFFPYIKTRVNVTHKEEILTL	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLG	SV
HC5	MHAFPPYIKTRISVIQKEEFVLT	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLG	SV

Coiled-Coil 2

HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKKVLLKEVFRQFVEACGQ	LAVNERLIKEDOLE
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKKVLLKEVFRQFVEACGQ	LAVNERLIKEDOLE
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKKVLLKEVFRQFVEACGQ	LAVNERLIKEDOLE
HC4	SVQVNAGPLAYARAFLLDDTNTKRYPDNKKVLLKEVFRQFVEACGQ	LAVNERLIKEDOLE
HC1	SVQVNAGPLAYARAFLLDDTNTKRYPDNKKVLLKEVFRQFVEACGQ	LAVNERLIKEDOLE
HC3	SVQVNAGPLAYARAFLLDDTNTKRYPDNKKVLLKEVFRQFVEACGQ	LAVNERLIKEDOLE
HC5	GTTVNQGFLEVAQVFLAEIPADFCLYRHHNKLRLCFKDFPKRCEALRNKNSLIGPVQKE	VEKNKRILITADORE

Coiled-Coil 2

HC2A	YQEEMKANYREMAKELSEIMH	ICPLEEKTSS-VLPNSLHIFNAISGTPSTMTVMHGMTSS
KIAA	YQEEMKANYREMAKELSEIMH	ICPLEEKTSS-VLPNSLHIFNAISGTPSTMTVMHGMTSS
rat	YQEEMKANYREMAKELSEIMH	ICPLEEKTSS-VLPNSLHIFNAISGTPSTMTVMHGMTSS
HC4	YHGLKSNFRDMVKELSDIIE	ILQEDTMHSPWMSNTLHVFCASIGTSSDRGYGSPRYA
HC1	YHGLKSNFRDMVKELSDIIE	ILQEDTMHSPWMSNTLHVFCASIGTSSDRGYGSPRYA
HC3	YHGLKSNFRDMVKELSDIIE	ILQEDTMHSPWMSNTLHVFCASIGTSSDRGYGSPRYA
HC5	YQELKKNYNKLNKENLRPMIER	KIPELYKPIRVESQKRSDFHRSSFRKCEQTLSQGS--

PBM

HC2A	SSVV	-----
KIAA	SSVV	-----
rat	SSVV	-----
HC4	SSVV	-----
HC1	SSVV	-----
HC3	SSVV	-----
HC5	SSVV	-----

HC2A	----
KIAA	----
rat	VHIFF
HC4	----
HC1	----
HC3	----
HC5	----

FIG. 3A (5 of 5)

	A	B
CLASP-1	YRVAFYQ:::GFFEEDGKEYIYKEP	
KIAA1058	FRVAFFGQAQYQFTDSETOVEGFFEDEGKEYIYKEP	
CLASP-2	FEDEEDGKEYIYKEP	
CLASP-6	FRVAFFGQ:::GFFEEDGKEYIYKEP	
CLASP-4	FRVAFYQ:::SFFEEDGKEYIYKEP	
DOCK180	FVGVYQ:::GFTFLRGKVFYRGKEYERRERED	
DOCK2	FVGVYQ:::GFTFLRGKVFYRGKEYERRERED	
DOCK3	FRVGFYGR:::KFPFLRNKEFVCRSH	
KIAA0716	FRVGFYGR:::KFPFLRNKEFVCRSH	
CLASP-3	FRVGFYGT:::KFGDLDEQEFVYKEP	
CONSENSUS	F V FYG	KEY K Q E R

	C
TRG	PKLTPLSEISQRLLKLYADKFGADNVKIIQDSGNVKNPKDLDGKFAVIQVTHVTFEFDKE
CLASP-1	PKLTGLSEISQRLLKLYADKFGADNVKIIQDSGNVKNPKDLDGKFAVIQVTHVTFEFDKE
CLASP-2	PKLTPLSEISQRLLKLYADKFGADNVKIIQDSGNVKNPKDLDGKFAVIQVTHVTFEFDKE
CLASP-4	PKLTGLSEISQRLLKLYADKFGADNVKIIQDSGNVKNPKDLDGKFAVIQVTHVTFEFDKE
CLASP-3	PAITKLAELSHRIEFGGKFGEDVVEVVKDSNPVDCKLDPNKAYIQITVVEPYFTYE
KIAA0716	HDYERLEAFQGRMLNEFPFAIA-----MQHANQFDETFQAEQYLCIYAVTPIPTQSE
DOCK3	HDYERLEAFQGRMLNEFPFAIA-----MQHPNHPDDAILQCDAQYLCIYAVTPIPTQVD
DOCK2	FQMQLMTQFPNAEK-----MNTTSAPGDVVKNAFGQYIQCFTVQPVLDCHP
DOCK180	EYERREDFQMQLMTQFPNAEK-----MNTTSAPGDVVKNAFGQYIQCFTVQPVLDCHP
CONSENSUS	L L Y M F

	D	E
CLASP-1	RTILPTSHIFPYVKRIQVVISQSSTELNPIEVAIDEMSRKVSELN	
TRG	RTILTAIHCFPYVKRIQVVISQSSTELNPIEVAIDEMSKKVSELN	
KIAA1058	RTILTAIHCFPYVKRIQVVISQSSTELNPIEVAIDEMSKKVSELN	
CLASP-2	RTILTAIHCFPYVKRIQVVISQSSTELNPIEVAIDEMSKKVSELN	
CLASP-6	RTILTAIHCFPYVKRIQVVISQSSTELNPIEVAIDEMSKKVSELN	
CLASP-4	RTILTTNSHFPYVKRIQVVISQSSTELNPIEVAIDEMSKKVSELN	
CLASP-3	RTILTTNSHFPYVKRIQVVISQSSTELNPIEVAIDEMSKKVSELN	
CLASP-5	RTILTTNSHFPYVKRIQVVISQSSTELNPIEVAIDEMSKKVSELN	
KIAA0716	RTSINLVQSLPGISRWFVEVVKRVEVMSPLENAIETMSANEKIL	
DOCK2	RTSINLVQSLPGISRWFVEVVKRVEVMSPLENAIETMSANEKIL	
DOCK3	RTSINLVQSLPGISRWFVEVVKRVEVMSPLENAIETMSANEKIL	
DOCK180	RTSINLVQSLPGISRWFVEVVKRVEVMSPLENAIETMSANEKIL	
CONSENSUS	RT L PP V + V + P+E A+ M +L E L L + I	

FIG. 3B (1 of 2)

	F	G			
CLASP-1	SLQLKLQGSVSQVKNAGPMAYARAFLEETNAKKYEDNKV--KILKEIFRQFADACGQALD				
TRG	KLQLKLQGSVSQVKNAGPLAYARAFLEDDNTKRYEDNKV--KILKEVFRQFVEACGQALA				
KIAA1058	KLQLKLQGSVSQVKNAGPLAYARAFLEDDNTKRYEDNKV--KILKEVFRQFVEACGQALA				
CLASP-2	KLQLKLQGSVSQVKNAGPLAYARAFLEDDNTKRYEDNKV--KILKEVFRQFVEACGQALA				
CLASP-6	KLQLKLQGSVSQVKNAGPLAYARAFLEDDNTKRYEDNKV--KILKEVFRQFVEACGQALA				
CLASP-3	MLQMVLQGSVGTTVNQGPLEYAQVFLSE--IPSDPKLFRHHNRLRLCFKDFTKRCEDALR				
CLASP-4	KLQLKLQGSVSQVKNAGPLAYARAFLEDDNTKRYEDNKV--KILKEVFRQFVEACGQALA				
CLASP-5	MLQMVLQGSVGTATVNQGPLEYAQVFLSE--IPADPKLYRHHNRLRLCFKEFIMRCGSAVE				
KIAA0716	ELTMCLNGVIDAAVNGGFSRYQEAFVFRSYILSHPEDEGKIARLRLEMLSEQAQLFEGLA				
DOCK2	FLSMMLNGIVDPAVMGGFARYEKAFFTESYVRDHPEDQDKLTHKDLIAWQIPFLGAGIK				
DOCK3	ILSMCLNGVIDAAVNGGFIARYEKAFFDRDYINKHPSDAEKITQLKELMQEQVHVLGVGLA				
DOCK180	FLSMMLNGIVDPAVMGGFARYEKAFFTESYVRDHPESAHEKIEHLKDLIAWQIPFLAEGIR				
CONSENSUS	L M L+G V VN G Y AFL + B L				
	L I V V F + I				

DOCK2-KIAA0209

DOCK3-KIAA0299

CLASP2variant-KIAA1058

FIG. 3B (2 of 2)

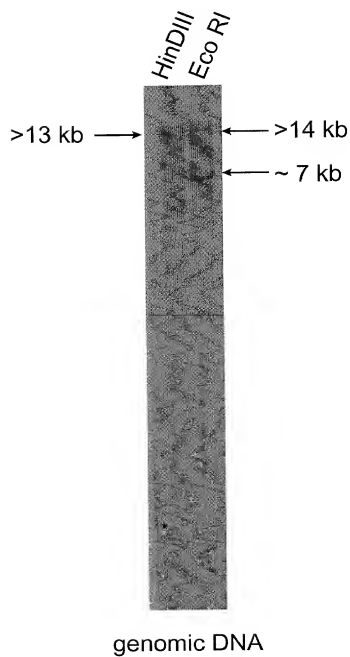


FIG. 4

-12 -1
GACGCGAGGACG

1/1 31/11
ATG GCT GCC TCC GAG CGC CGC GGC TTC GCG CAC AAG ATC AAC AGG AGC GTG GCC GCA GAG
Met ala ala ser glu arg arg ala phe ala his lys ile asn arg thr val ala ala glu
61/21 91/31
GTG CGG AAG CAG GTG TCC CGG GAA CGC AGT GGC TCC CCC CAC TCC AGC AGG CGC TGC AGC
val arg lys gln val ser arg glu arg ser gly ser pro his ser ser arg arg cys ser
121/41 151/51
AGC TCC CTG GGG GTC CCA CTG ACT GAA GTT GTC GAG CCC CTG GAC TTT GAG GAT GTA CTT
ser ser leu gly val pro leu thr glu val val glu pro leu asp phe glu asp val leu
181/61 211/71
CTG AGC CGG CCA CCA GAT GCT GAG CCC GGG CCC CTC AGG GAC CTG GTA GAA TTC CCA GCT
leu ser arg pro pro asp ala glu pro gly pro leu arg asp leu val glu phe pro ala
241/81 271/91
GAT GAC TTG GAG CTG CTG CTG CAG CCC CGG GAA TGC CGG ACC AGC GAG CCC GGG ATC CCC
asp asp leu glu leu leu leu gln pro arg glu cys arg thr thr glu pro gly ile pro
301/101 331/111
AAG GAT GAA AAA CTG GAT GCC CAG GTG AGG GCG GCG GTG GAG ATG TAT ATT GAG GAC TGG
lys asp glu lys leu asp ala gln val arg ala ala val glu met tyr ile glu asp trp
361/121 391/131
GTC ATT GTC CAC AGA AGG TAT CAG TAC CTG AGT GCA GCA TAC AGC CCC GTC ACC ACA GAC
val ile val his arg arg tyr gln tyr leu ser ala ala tyr ser pro val thr thr asp
421/141 451/151
ACA CAG CGG GAG CGA CAG AAG GGC CTC CCC CGC CAG GTC TTT GAG CAG GAT GCT TCT GGA
thr gln arg glu arg gln lys gly leu pro arg gln val phe glu gln asp ala ser gly
481/161 511/171
GAC GAG AGG TCC GGC CCT GAG GAC TCG AAT GAC TCC CGG CGT GGC TCG GGC TCC CCG GAA
asp glu arg ser gly pro glu asp ser asn asp ser arg gly ser gly ser pro glu
541/181 571/191
GAC ACC CTT CGA AGC AGT GGT GCC TCT AGC ATC TTC GAC CTG AGG AAC CTG GCA GCT GAC
asp thr pro arg ser ser gly ala ser ser ile phe asp leu arg asn leu ala ala asp
601/201 631/211
TCA TTG CTG CCC TCT CTG CTA GAG CGG GCG GCC CCA GAA GAT GTG GAC CGG CGC AAT GAA
ser leu leu pro ser leu leu glu arg ala ala pro glu asp val asp arg arg asn glu
661/221 691/231
ACC CTT CGA CGG CAG CAC CGG CCC CCG GCC CTG CTC ACC CTC TAC CCG GCA CCT GAC GAG
thr leu arg arg gln his arg pro pro ala leu leu thr leu tyr pro ala pro asp glu
721/241 751/251
GAT GAA GCC GTG GAA CGC TGT AGC CGC CCA GAG CCA CCC CGC GAG CAC TTT GGA CAA AGG
asp glu ala val glu arg arg cys ser arg pro glu pro pro arg glu his phe gly gln arg
781/261 811/271
ATC TTG GTC AAG TGT CTG TCG CTC AAG TTC GAG ATT GAA ATT GAG CCC ATC TTT GGG ATC
ile leu val lys cys leu ser leu lys phe glu ile glu ile glu pro ile phe gly ile
841/281 871/291
TTG GCT CTG TAT GAT GTG CGG GAG AAA AAG AAG ATC TCG GAG AAC TTC TAC TTC GAC CTG
leu ala leu tyr asp val arg glu lys lys lys ile ser glu his phe phe asp leu
901/301 931/311
AAC TCG GAC TCC ATG AAG GGG CTG CTT CGG GCT CAT GGC ACC CAC CCT GCC ATC TCC ACC
asn ser asp ser met lys gly leu leu arg ala his gly thr his pro ala ile ser thr
961/321 991/331
CTG GCC CGC TCT GCC ATC TTC TCT GTG ACC TAC CCC TCA CCT GAC ATC TTC CTG GTC ATC
leu ala arg thr asp thr ala lys asn lys glu lys leu glu lys leu arg leu ala ala
1021/341 1051/351
AAG TTG GAG AAG GTG CTT CAG CAA GGG GAC ATC AGT GAG TGC TGT GAG CCT TAC ATG GTG
lys leu glu lys val leu gln gln gly asp ile ser glu cys cys glu pro tyr met val
1081/361 1111/371
TTG AAA GAA GTG GAC ACA GCC AAG AAC AAA GAG AAG CTA GAG AAG CTG CGC CTG GGC GCC
leu lys glu val asp thr ala lys asn lys glu lys leu glu lys leu arg leu ala ala

FIG. 5A(1 of 6)

1141/381
GAG CAG TTC TGC ACC CGC CTG GGC CGC TAC
glu gln phe cys thr arg leu gly arg tyr
1201/401
TTG GCC AAC ATC GTG AGC AGC GCT GGC CAG
leu ala asn ile val ser ser ala gly gln
1261/421
CGC CGS CCA GCC TGG ACA GAC CGC CGC CGT
arg arg pro ala trp thr asp arg arg arg
1321/441
GAC GAC GCC TGC AGC TTC TCT GGC TTC CGT
asp asp ala cys ser phe ser gly phe arg
1381/461
AAG CAG GAG GCT GAG CGA CTC AGT GAC GAG
lys gln glu ala glu arg leu ser asp glu
1441/481
CGC CGG TCG TCC CTG CTG CGG CGA CTA CGT
arg pro ser ser leu leu arg arg leu arg
1501/501
TCT CCG GCT CCT GAA AAT CCC CAC TTC TGC
ser pro ala pro glu asn pro his phe cys
1561/521
TAC CCG GAC CCC AGG GGC CGG CCC ACC AAG
tyr pro asp pro arg gly arg pro thr lys
1621/541
TAT GCC CCC CAT ACC AGC TAC AGS AAC CTG
tyr ala pro his thr ser tyr arg asn leu
1681/561
AGC AGC CGC CAG GGC TCC GTG CGC AAC CTT
ser ser arg gln gly ser val arg asn leu
1741/581
GAC CCC AGC CAG GCT CTG CCG GTC ATC TTT
asp pro ser gln ala leu pro val ile phe
1801/601
GAG GCC TTC ACA CCG GTG GTC TAC CAT AAC
glu ala phe thr pro val val tyr his asn
1861/621
CTG CAT CTT CCA GCC TGC GTG ACA GAG AAC
leu his leu pro ala cys val thr glu asn
1921/641
AGC TGC CAG CCC CGG CCG GGC ACT GCC CTG
ser cys gln pro arg pro gly thr ala leu
1981/661
CTG CTG CAG CAC GGC CGC CTG AGG ACC GGC
leu leu gln his gly arg leu arg thr gly
2041/681
CCG CCG CCC AGC TAT TCC GTG CTC ACA CCC
pro pro pro ser tyr ser val leu thr pro
2101/701
GAC GGT CAC AAG GGC GTG TTC AGT GTG GAG
asp gly his lys gly val phe ser val glu
2161/721
GAC CCC TAC CTG GAC AAA TTC TTC ACC CTG
asp pro tyr leu asp lys phe phe thr leu
2221/741
TTC CGG CTC AAG GAC ACT GTG CTG AGC GAG
phe arg leu lys asp thr val leu ser glu
1171/391
CGC ATG CCC TTC GCC TGG ACG GCC GTG CAC
arg met pro phe ala trp thr ala val his
1231/411
CTG GAC CGG GAC TCT GAC TCG GAG GGC GAG
leu asp arg asp ser asp ser glu gly glu
1291/431
CGG GGG CCC CAG GAC CGG GCG AGT AGT GGG
arg gly pro gln asp arg ala ser ser gly
1351/451
CCA GCC ACG CTA ACT GTC ACA AAC TTC TTT
pro ala thr leu thr val thr asn phe phe
1411/471
GAC CTC TTC AAG TTC CTG GCT GAC ATG AGG
asp leu phe lys phe leu ala asp met arg
1471/491
CCT GTG ACT GCC CAG CTC AAG ATC GAC ATT
pro val thr ala gln leu lys ile asp ile
1531/511
CTC TCC CCT GAG CTG CTT CAT ATC AAG CCC
leu ser pro glu leu leu his ile lys pro
1591/531
GAG ATT CTG GAC TTC CCC GCC CGC GAA GTC
glu ile leu glu phe pro ala arg glu val
1651/551
CTG TAC GTG TAC CCG CAC AGC CTC AAC TTC
leu tyr val tyr pro his ser leu asn phe
1711/571
GCT GTG CGA GTG CAG TAC ATG ACA GGC GAG
ala val arg val gln tyr met thr gly glu
1771/591
GGC AAG TCC AGC TGC AGT GAA TTT ACC CGC
gly lys ser ser cys ser glu phe thr arg
1831/611
AAG TCC CCC GAG TTC TAC GAG GAG TTC AAG
lys ser pro glu phe tyr glu glu phe lys
1891/631
CAT CAC CTG CTG TTC ACC TTC TAC CAT GTC
his his leu leu phe thr phe tyr his val
1951/651
GAG ACA CCC GTG GGC TTT ACT TGG ATC CCA
glu thr pro val gly phe thr trp ile pro
2011/671
CCC TTC TGT CTC CCA GTG TCT GTG CAC CAG
pro phe cys leu pro val ser val asp gln
2071/691
GAT GTG CGC CTT CCG GGC ATG CGC TGG GTG
asp val ala leu pro gly met arg trp val
2131/711
CTC ACA GCC GTG TCC TCT GTG CAC CCC CAG
leu thr ala val ser ser val his pro gln
2191/731
GTG CAC GTC CTG GAG GAG GGA GCC TTC CCA
val his val leu glu glu gly ala phe pro
2251/751
GGC AAC GTG GAG CAG GAG CTG CGG GCC AGT
tyr arg leu lys asp thr val leu ser glu
gly asn val glu gln glu leu arg ala ser

FIG. 5A (2 of 6)

2281/761
 CTT GCA GCA CTG CGC CTG GCC AGC CCC GAA
 leu ala ala leu arg leu ala ser pro glu
 2341/781
 GAC AAG CTC GTG CGT CTG GTC ATC AGG CCC
 asp lys leu val arg leu val ile arg pro
 2401/801
 GGC CGT GGA GCC TTT GAA GCA ATG GCC CAT
 gly arg gly ala phe glu ala met ala his
 2461/821
 GCA GCC CAG GAT GCC CGC GGT CAC TGC CCA
 ala ala gln asp ala arg gly his cys pro
 2521/841
 CGC CTT CCT GGC ACT GAG CCC AGC CTC CCG
 arg leu pro gly thr glu pro ser leu pro
 2581/861
 GCC ACA CTG GCC CGT GGC TCT GGT CGC CCC
 ala thr leu ala arg gly ser gly arg pro
 2641/881
 ATC AGC AGC AGC AAC CCT GAC CTC GCC GTG
 ile ser ser ser asn pro asp leu ala val
 2701/901
 CGC ATC CTG GCC AGC AGG CTG CTT CAC GAG
 arg ile leu ala ser lys leu leu his glu
 2761/921
 AGT GCC GTA CGC GAG GCC ATC CTC CAG CAC
 ser ala val arg glu ala ile leu gln his
 2821/941
 AGT ATG CGC CTG CAC CTG CTG CTT GGC CAG
 ser met ala leu his leu leu leu gly gln
 2881/961
 CCC GGA CGC TTC CTG GAC GAC ATC ACT GCC
 pro gly arg phe leu asp asp ile thr ala
 2941/981
 ACC CGT GTC CAC AAG GAT GTG GAG CTG GCC
 thr arg val his lys asp val glu leu ala
 3001/1001
 CTC AGT GAC CTT CTG TCC CTG GTG GAC CGG
 leu ser asp leu leu ser leu val asp arg
 3061/1021
 TAC AAG CAG GAG GTG GCC ACG CGG CTC CAG TCG
 tyr lys gln val ala thr arg leu gln ser
 3121/1041
 CGC ATG GAA TTC ACC CGC ATC CTG TGC AGC
 arg met glu phe thr arg ile leu cys ser
 3181/1061
 TGC TGC CCC CTG TCA CCT CCA GCC TGC CCC
 cys cys pro leu ser pro pro ala ser pro
 3241/1081
 AGC TCC ACC TTC TCC AGC CAA GCC CCG GAC
 ser ser thr phe ser ser gln ala pro asp
 3301/1101
 GGA CCA TTC CGG CAG CAG CAC TTC CTA GCT
 gly pro phe arg gln gln his phe leu ala
 3361/1121
 CTC GAA CCT GAG GCT GAA GGG CCA TTC CTG
 leu glu pro glu ala glu gly ala phe leu
 3421/1141
 AGC CTG CTA TGT GGC CAT GAC ACT GAC CCC
 ser leu leu cys gly his asp thr asp pro
 3481/1161
 GAG GAG CTG TAC CTG CCA CTG CTT TCG ATT
 val ala glu leu tyr leu pro leu leu ser
 2311/771
 CCC CTT GTG GCC TTC TCC CAC CAC GTG CTG
 pro leu val ala phe ser his his val leu
 2371/791
 CCG ATC ATC AGT GGC CAG ATT GTG AAC CTG
 pro ile ile ser gly gln ile val asn leu
 2431/811
 CTA GTC AGC CTT GTT CAC CGG AGC CTG GAG
 val val ser leu val his arg ser leu glu
 2491/831
 CAG CTG GCT GCC TAC GTC CAC TAC GCC TTT
 gln leu ala ala tyr val his tyr ala phe
 2551/851
 GAT GGG GCC CCT CCA GTG ACA GTG CAG GCT
 asp gly ala pro pro val thr val gln ala
 2611/871
 GCA AGC CTC TAC CTG CGC CGT TCC AAG AGC
 ala ser leu tyr leu ala arg ser lys ser
 2671/891
 GCC CCT GGC TCT GTG GAT GAG GAG GTT TCC
 ala pro gly ser val asp gly val ser
 2731/911
 GAG CTG GCT CTG CAG TGG GTG GTC AGC AGC
 glu leu ala leu gln trp val val ser ser
 2791/931
 GCC TGG TTC TTC TTC CAG CTC ATG GTG AAG
 ala thr phe phe phe gln leu met val lys
 2851/951
 CGA CTA GAC ACA CCC CGC AAG CTG CGC TTC
 arg leu asp thr pro arg lys leu arg phe
 2911/971
 TTG GTG GGC TCT GTG GGC CTG GAG GTC ATC
 leu val gly ser val gly leu glu val ile
 2971/991
 GAG CAC CTC AAC GCC AGC CTG GCT TTC TTC
 glu his leu asn ala ser leu ala phe phe
 3031/1011
 GGC TTT GTC TTC AGC CTG GTC CGG GCC CAC
 gly phe val phe ser leu val arg ala his
 3091/1031
 TCC CCT AAT CCA GCA GCC CTG CTG ACC CTG
 ser pro asn pro ala ala leu leu thr leu
 3151/1051
 CAC GAG CAC TAC GTG ACC CTC AAC CTC CCC
 his glu his tyr val thr leu asn leu pro
 3211/1071
 TCC CCC TCT GTG TCC TCC ACC ACC TCC CAG
 ser pro ser val ser ser thr thr ser gln
 3271/1091
 CCC AAG GTG ACC AGC ATG TTC GAA CTC AGT
 pro lys val thr ser met phe glu leu ser
 3331/1111
 GGG CTC CTG CTG ACG GAG CTG GCA CTG GCC
 gly leu leu leu thr glu leu ala leu ala
 3391/1131
 TTG CAC AAG AAG GCC ATC AGT GCT GTG CAC
 leu his lys lys ala ile ser ala val his
 3451/1151
 CGC TAC GCC GAG GCC ACT GTG AAG GCT CGT
 arg tyr ala glu ala thr val lys ala arg
 3511/1171
 GCG GAG GAT ACC TTG CCA CGG CTG CAT
 val ala glu leu tyr leu pro leu leu ser
 ile ala arg asp thr leu pro arg leu his

FIG. 5A (3 of 6)

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3541/1181
GAC TTT GCT GAG GGC CCA GGT CAG CGS TCA
asp phe ala glu gly pro gly gln arg ser
3601/1201
GAA GGC GAA GGG GAC ATT GCG GGT ACC ATC AAC CCC TCT GTG GCC ATG GCC ATT GCT GGT
glu gly glu gly leu asp ile ala gly thr ile
3661/1221
GGC CCC CTA GCC CCT GGC TCC CGS GCC AGC
gly pro leu ala pro gly ser arg ala ser
3721/1241
GCA GGC TGT GCC CTC TCT GCT GAG TCA AGC
ala gly cys ala ile leu ser ala glu ser ser
3781/1261
CTG AAA AAC ACC GAG CCG GCG CTC CTG CAG
leu lys asn thr glu pro ala leu leu gln
3841/1281
CTG GGA CGT CTG TTG GAC TTG CTG TAC CTT
leu gly cys ala ile leu asp leu leu tyr leu
3901/1301
AAG GCC TTT GAA CGC ATC AAC AGC CTC ACA
lys ala phe glu arg ile asn ser leu thr
3961/1321
CTA GAG GAA GCC ATT CTG GGT ACC ATC GGA
leu glu glu arg leu leu leu gly thr ile gly
4021/1341
GAG AGG AGC CCG TTT GGG AAT CCA GAG AAC
glu arg ser pro phe gly asn pro glu asn
4081/1361
AAG CAA ACC TCA GAC CGC GTG GAC AAG ACC
lys gln thr val ser asp arg val asp lys thr
4141/1381
GAA GGG AAC CTG GCA ACC GAG GCA AGC CTA
glu gly asn leu ala thr glu ala ser leu
4201/1401
CAG ACG GTG ATG CTT TCA GAA GCC CGG GAG
gln thr val met leu ser glu ala arg glu
4261/1421
CTG TAC AGC CTG GGC AGT GCC CAG AGT GCC
leu tyr ser leu gly ser ala gln ser ala
4321/1441
AGG GCC CTT GTG TCC AAG TTC CCG GAG CTG
arg ala leu val ser lys phe pro glu leu
4381/1461
GAC CTG TGC CTG AGG CTC CTA CGA CAC TGT
asp leu cys leu arg leu leu arg his cys
4441/1481
GCC AGC GCC TCG CTG TAC CTG CTC ATG CGA
ala ser ala ser leu tyr leu leu met arg
4501/1501
CGT GTG AAG ATG CAG GTC ACC ATG TCT CTC
arg val lys met gln val thr met ser leu
4561/1521
AGT GAA GAG CAC CTG CGA CGT TCA CTC AAA
ser glu glu his leu arg arg ser leu lys
4621/1541
GGG CTG CGG GAG ACC ACC TTC GCA GAG CAG
gly leu arg asp ser thr phe ala glu gln
4681/1561
ATC CTG AGC GAG ACG GTC AAG ATG AAG GAA
ile leu thr asp thr val lys met lys glu
3571/1191
AGA CTG GCC TCA ATG CTT GAC TCA GAC ACA
arg leu ala ser met leu asp ser asp thr
3631/1211
AAC CCC TCT GTG GCC ATG GCC ATT GCT GGT
asn pro ser val ala met ala ile ala gly
3691/1231
ATC TCC CAG GGG CCA CCA ACG GCT TCT CGC
ile ser gln gly pro pro thr ala ser arg
3751/1251
CGG ACC TTG CTG GCG TGT GTG CTG TGG GTG
arg thr leu leu ala cys val leu trp val
3811/1271
CGC TGG GCC ACT GAC CTG ACA CTC CCC CAG
arg trp ala thr asp leu thr leu pro gln
3871/1291
TGC CTG GCT GCC TTT GAG TAC AAG GGG AAA
cys leu ala ala phe glu tyr lys gly lys
3931/1311
TTC AAA AAA TCT CTG GAT ATG AAG GCG CGG
phe lys lys ser leu asp met lys ala arg
3991/1331
GCT CGA CAA GAA ATG GTT CGG CGA AGT CGT
ala arg gln glu met val arg arg ser arg
4051/1351
GTG CGC TGG CGG AAG AGC GTC ACA CAC TGG
val arg trp arg lys ser val thr his trp
4111/1371
AAG GAT GAA ATG GAA CAC GAG GCC TTG GTG
lys asp glu met glu his gly ala leu val
4171/1391
GTG GTT CTG GAC ACA CTG GAG ATC ATC GTG
val val leu asp thr leu glu ile ile val
4231/1411
AGC CTC TTG GGG GCA CTG CTG AAG GTT GTG
ser val leu gly ala val leu lys val val
4291/1431
CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG
leu phe leu gln his gly leu ala thr gln
4351/1451
CTG TTC GAG GAG CAC ACG GAG CTG TGT GCC
leu phe glu glu asp thr glu leu cys ala
4411/1471
GGC AGC CGC ATC AGC ACC ATC CGC AGC CAC
gly ser arg ile ser thr ile arg thr his
4471/1491
CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC
gln asn phe glu ile gly his asn phe ala
4531/1511
TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC
ser ser leu val gly thr thr gln asn phe
4591/1531
ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG
thr ile leu thr tyr ala glu glu asp met
4651/1551
GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG
val gln asp leu met phe asn leu his met
4711/1571
CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC
cag cag gag cct gag atg atc atc gac

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FIG. 5A (4 of 6)

4741/1581
CTC ATG TAC AGA ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG
leu met tyr arg ile ala arg gly tyr gln gly ser pro asp leu arg leu thr trp leu
4801/1601
CAG AAC ATG GCC GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC CAG TGC ATG
gln asn met ala gly lys his ala glu leu gly asn his ala glu ala ala gln cys met
4861/1621
GTG CAC GCG GCC GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAG CGC CAC CTG
val his ala ala ala leu val ala glu tyr leu ala leu leu glu asp gln arg his leu
4921/1641
CCC GTG GGC TGC GTT TCC TTC CAG AAC ATC TCA TCC AAC GTG CTA GAG GAG TCC GCC ATC
pro val gly cys val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile
4981/1661
TCC GAC GAC ATC CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG
ser asp asp ile leu ser pro asp glu glu gly phe cys ser gly lys his phe thr glu
5041/1681
CTG GGG CTG GTA GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC
leu gly leu val gly leu leu glu gln ala ala gly tyr phe thr met gly gly leu tyr
5101/1701
GAG GCG GTG AAT GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC
glu ala val asn glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr
5161/1721
AAG AAG CTG GCC GCG GTG CAC GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG
lys lys leu ala ala val his gly lys leu gln glu ala phe thr lys ile met his gln
5221/1741
AGT TCC GGC TGG GAG CGC GTG TTC GGC ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC
ser ser gly trp glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his
5281/1761
TTC GGT GAC CTG GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA
phe gly asp leu asp gly gly leu glu phe val tyr lys glu pro ser ile thr lys leu ala
5341/1781
GAG ATC TCA CAC CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG
glu ile ser his arg leu glu glu phe tyr thr glu arg phe gly asp asp val val glu
5401/1801
ATT ATC AAA GAC TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC
ile ile lys asp ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile
5461/1821
CAG ATC ACG TAT GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC
gln ile thr tyr val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr
5521/1841
TTT GAC CGC AAC TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG
phe asp arg asn tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly
5581/1861
CGC GCA CAC GGG GAG CTG CCC GAG CAA CAC AAG COT AAG ACG CTG CTC AGC ACC GAC CAC
arg ala his gly leu glu pro glu gln his lys arg lys thr leu leu ser thr asp his
5641/1881
GCC TTC CCC TAC ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG
ala phe pro tyr ile lys thr arg ile arg val cys his arg glu glu thr val leu thr
5701/1901
CCA GTG GAG GTG GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC
pro val glu val ala ile glu asp met gln lys lys thr arg glu ala phe ala thr
5761/1921
GAG CAG GAC CCA CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC
glu gln asp pro pro asp ala lys met leu gln met val leu gln gly ser val gly pro
5821/1941
ACC GTG AAC CAG GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC
thr val asn gln gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp
5881/1961
CCC AAG CTC TCT CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA
pro lys leu phe arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys

FIG. 5A (5 of 6)

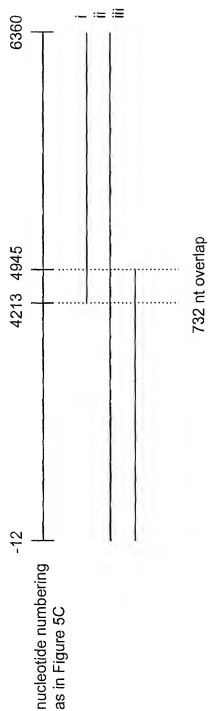
5941/1981
 TGT GAG GAT GCG CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC
 cys glu asp ala leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his
 6001/2001
 CGT GAG CTG GAG CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG
 arg glu leu glu arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln
 6061/2021
 CGC CTG CCC CAG CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA
 arg leu pro gln leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala
 6121/2041
 AGT TTC CGA AAG GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG
 ser phe arg lys ala asp leu OPA
 6181/2061
 CAC CCG GGC CTC AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT
 6241/2081
 GGG GTG ACC ACA CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA
 6301/2101
 CTG ATG CTT CCT CCC TTT CTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA
 5971/1991
 6031/2011
 6091/2031
 6151/2051
 6211/2071
 6271/2091
 6331/2111

FIG. 5A (6 of 6)

A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-7 cDNA isoforms

isoform	Nucleotide(s)	Consequence
1	1993	G to A; glycine to arginine
2	2136	A to G; missense
3	3166	A to G; threonine to alanine
4	3902	A to T; lysine to methionine
5	3918	C to T; missense
6	3937	A to C; lysine to glutamine
7	4002	A to C; glutamic acid to aspartic acid
8	4017	T to A; serine to arginine
9	4020	T to C; missense
10	4034-5	TT to AC; phenylalanine to tyrosine
11	4911	G to C change; missense mutation changing codon from glutamine to histidine

These differences may be found separately or together in various combination in the difference human CLASP-7 isoforms



C

FIG. 5B (2 of 2)

Exon 63800 to 63920

GCGGGGCCGGGGCCGGGGCGGGCGGGACGGCAGGACCAATGGCTGC
CTCCGAGCGCGCGCCCTTCGCGACAAGATCAACAGGTAGTGTGGCCGCGGG
CCCCCTCCCACTCCC

Exon 72530 to 72670

CCAAATGGCCCCCTCCCTATCTTTCCAGGACGGTGGCCGAGAGGTGCGGAAG
CAGGTGTCCCGGGAACGCAGTGGCTCCCCCACTCCAGCAGGCGCTGCAGCA
GCTCCCTGGGGGTAAATATTGGGGGTCCGCCCCA

Exon 73300 to 73530

TCACAGCCACTTTGCTCCAATCCAGGTCCCACTGACTGAAGTTGTCGAGCCCC
TGGACTTTGAGGATGACTTCTGAGCCGGCCACCAGATGCTGAGCCCGGGCC
CCTCAGGGACCTGGTAGAATCCCACTGATGACTTGGAGCTGCTGCTGCAG
CCCCGGGAATGCCGGACCAACGGAGCCGGATCCCCAAGGATGAGTGGGTTC
AGCCCCACGCCCTCTCTGCCTG

Exon 73700 to 73830

GTCTCTGTTTACCTGATCTTCTTTTGCTGCAGAAACTGGATGCCCAGGTGA
GGCCGCGGTGGAGATGTATATTGAGGACTGGGTATTGTCCACAGAAGGTG
AGTCTGACTTAGGGGCAGCTCAGGGG

Exon 74010 to 74190

CCTGCCAGCCCCGTTTCCGCTAGGTATCAGTACCTGAGTGACGATACAGC
CCCGTCACCACAGACACACAGCGGGAGCGACAGAGGGCCCTCCCCCGCCAG
GTCTTTGACAGGATGCTTCTGAGACGAGAGGTCCGGCCCTGAGGACTCGG
TGAGGAAGCCCTGGCTGGGGTAC

Exon 75170 to 75450

CAGTGCTTGACATTCTCCACTGGCAGAACTGACTCCGGCGTGGCTCGGCTC
CCCGGAAGACACCCCTCGAAGCAGTGGTGCCTTAGCATCTTCGACCTGAGG
AACCTGGCAGCTGACTCATTTGCTGCCCCCTCTGCTAGAGCGGGCGGCCAG
AAGATGTGGACCGGCGCAATGAACCCCTTCGACGGCAGACACCGCCCCCGGC
CCTGCTCACCTCTACCCGGCACCTGACGAGGTGGGTGCCCTTCCAGATAT
CAGCCAACCAAGCATTTACT

FIG. 6A (1 of 7)

Exon 78100 to 78250

CCGCCCCAGCTCCACCCCCCACTCTTGGCAGGATGAAGCCGTGGAACGCTG
TAGCCGCCAGAGCCACCCTGGCAGACCTTTGGACAAGGATCTTGGTCAAG
TGTCTGTGCTCAAGTGAGTATACTGACATGCTCTCTCTTAGATG

Exon 80380 to 80500

CCCCCTCCCTCCCATTTACTTGTAGGTTGAGATTGAAATTGAGCCCATCTTT
GGGATCTTTGGCTCTGTATGATGTGCGGGAGAAAAAGAGGTAGGAGGCCCTT
TTTCTCTTCTCTCC

Exon 80540 to 80750

GTGCTGCCAGCTGCCCTCTGGTGTCCCCAGATCTCGGAGAAGTTCTACTTCG
ACCTGAACTCGGACTCCATCAAGGGCTGCTTCGGGCTCATSSCACTGCCATCTCCACC
CTGGCCCCGCTCTGCCATCTTCTCTGTGACCTACCCCTCACC
TGACATCTTCTGGTCATCAAGTGCCCTGCTGGGGCTGGGCAAGGGGTGGT

Exon 82370 to 82510

GCCTCACTGGATTCAATTCATCTGCCCCGAGTTGGAGAAGGTGCTTCAGCAAG
GGGACATCAGTGAAGTCTGTGAGCCCTACATGGTGTGAAAGAAGTGGACAC
ACCCAAGSTAAGCGTGTGGAGGCTGGACTAGGGCA

Exon 82540 to 82760

GCTGAGCTGGCAGGGGACGGGGTCTCCCCACAGAACAAAGAGAAGCTAGAG
AAGCTGCGCCTGGCGGCCGAGCAGTCTGACCCCGCTGGGCCGCTACCGCA
TGCCCTTGCCCTGGACGGCCGTGCACCTTGGCCAACATCGTGAGCAGCGCTGG
CGAGCTGGACCGGGACTCTGACTCGGAGGGCGGTGAGGAGGCGGGGCTAAC
AGGCTTGGGCGGGG

Exon 82860 to 83060

CTTGGTCCCCCTTTTGTCAATTGTCATTCCTCCCCCTAGAGCGCCGGCCAGCCT
GGACAGACCGCCCGCTCGGGGGCCCCAGGACCGGGCGAGTAGTGGGGACGACG
CCTGCAGCTTCTCTGGCTCCGTCCAGCCACGCTAACTGTACAAAACCTTC
TTTAAGCAGGTGCTCTACCTCGGGCCAGGACTCTCCCACTCC

Exon 83100 to 83260

GCCCCGGCTGACGGGAGTGGGTCCCATGTAGGAGGCTGAGCGACTCAGTGAC
GAGGACCTCTTCAAGTTCTGGGCTGACATGAGGCGCCCGTCGTCCTGCTGGG
GCGACTACGTCCTGTGACTGTGCGTGGCACACCCCATACACAAGAAGTATC
ACTC

FIG. 6A (2 of 7)

Exon 84050 to 84270

GTGCAAACCGGTTCTTCCCTTCCCAGCCAGCTCAAGATCGACATTCTCCGG
CICCTGAAAAATCCCCACTTCTGCCTCTCCCTGAGCTGCTTCATATCAAGCCC
TACCCGGACCCAGGGGCCGGCCCAAGGAGATTCTGGAGTCCCCGCC
GCGAAGTCTATGCCCCCATACCACTACAGGTACGGCCTCTGGGGCCACG
 TGGGCATTGA

Exon 87940 to 88130

GCCCCGTGTCCTCTGACACCCCATCTGCCCCACAGGAACCTGCTGACG
TGTACCCGCACAGCCTCAACTTCAGCAGCCGCCAGGGCTCCGTGGCGAACCT
TGCTGTGGAGTGCAGTACATGACAGGCGAGGACCCAGCCAGGCTCTGCCG
GTCA GTGGCTGTGCCCAGGGAAGGGGGTAGGG

Exon 88140 to 88270

TGGCTCCCTCATGAATCCACTCTCCAGGTCACTTTGGCAAGTCCAGCTGCA
GTGAATTTACCCGCGAGGCCTTCACACCGGTGGTCTACCATAACAAGTATGT
 AGGGGACACGTGAGGAATTGGGG

Exon 88470 to 88680

GCCCCCAGCAGATCCCCCAGCCGATTTCTGCCAGGTCCCCGAGTTCTACGA
GGAGTTCAAGCTGCATCTCCAGCCTGCCTGACAGAGAACCATCACTGCTG
TTCACTTCTACCATGTCACTGCGCAACCCCGCGCGCACTGCCCTGCAAGAC
ACCCGTGGGCTTTACTGTGAGCGTCCCTCCCTCCCTCCCTGAGCCCTC
 T

Exon 88680 to 88870

TCGTCCCCAACCTGGCGCAGACCTGACCTCCAGCCTCTCCCAAGTGGATCC
CACTGCTGCAGCAGGGCGCCTGAGGACCGGCCCTTCTGTCTCCCAAGTGTCT
GTGGACCAGCGCCGCCAGCTATTCCGTGCTACACCCGATGTATGTGCCCT
 GAGACTCTGCTGCGCAATGCACTGTCCCCAG

Exon 89360 to 89530

CAGGGAGGGCTGACCAGTGCCCACTGGTGCTCCCTCCACAGGTGGCGCT
TCCGGGCATGCGCTGGGTGGACGGTACAGGGCGTGTCACTGTGGAGCTC
ACAGCCGTGCTCTGTGTCACCCCAAGTACGGGGTGGGCCGGGAACCAAGA
 GTCCCGCCTGCTCC

Exon 89660 to 89980

TTCATTCCCTGAGGCCCCACCTTGCTCACATCCATCCCTACCCAGGACCCCT
ACCTGGACAAATTTCTCACCTGGTGACGTCCTGGAGGAGGGAGCCTTCCC
ATTCCGGCTCAAGGACACTGTGCTGAGCAGGGCAACCTGGAGCAGGAGCTG
CGGGCCAGTCTTGACGACTGCGCTGGCCAGGCCGGAACCCCTTGTCGCTT
CTCCACCACCTGCTGGACAAGCTCGTGCCTCTGGTCACTAGGCCCCGATC
ATCAGTGGCCAGATTGGTAAGCGAATGTGGCTCAGACCTCAGTTTCCCCATC
CACATG

Exon 90480 to 90730

AGAGGCCTTGGGCCCTGGAACCTGACCTCTGCTCTGCCCTGCAGTGAACCTG
GGCCGTGGAGCCTTTGAAGCAATGGCCCATGTAGTCAGCCTTGTTCACCGGA
GCCTGGAGGCAGCCAGGATGCCCGCGTCACTGCCACAGCTGGCTGCCTA
CGTCCACTACGCCCTTTCGCTTCTTGGCACTGAGCCAGCCTCCCGGATGGT
AGTTTGTAGAAATCCCTGTGAGACGAGAAATATCTGGGAGAA

Exon 92870 to 93120

ATCACATCAGGTGGGTGGGTGGTTGACCCCTATTCACCTCCATCCTCAGGSGCCG
TCCAGTGACAGTGCAGGCTGCCACACTGGCCCCGTGGCTCTGGTTCGCCGCC
AAGCCTCTACCTGGCGGTTCCAAGAGCATCAGCAGCAGCAACCCCTGACCTC
GCCGTGGCCCCCTGGCTCTGTGGATGACGAGGTTTCCCGCATCTGTGGCAGCA
AGGTAGGGCAACGGGGGCCCTGGAAATCCAGCCTCAGTGGT

Exon 97210 to 97390

GGCACCTCGCACTCTGTGACCCCTGCCTCTGTCCCCAGCTGCTTCACGAGGAG
CTGGCTCTGCAGTGGTGGTGCAGCAGCAGTGGCGTACGCGAGGCCATCTCC
AGCACGCTGTGTTCTTCTTCCAGCTCATGGTGAACCCCTCCTCCTGCCTG
GTGGCAAGAGACCCCAAGTGGAG

Exon 98770 to 98990

CAAATCCCACCCACAGCCCTCTCACCCACCCCAAGGTGAAGAGTATGGCGC
TGCACCTGCTGCTTGGCCAGGCACTAGACACACCCCGAAGCTGCGCTTCCC
CGGACGCTTCTGGACGACATCACTGCCTTGGTGGGCTCTGTGGGCTGGAG
GTCACTACCCGTTGCCACAAGGTGAGAGATGCAAGGTCTCAATGTGGGAAGA
AACCTGAGGGAGG

Exon 103130 to 103340

GGGGCTGAGGTTTGGGTGTGTGGGTGACAGGCACCTGTGTCCCAGGATGT
GGAGCTGGCCGAGCACCTCAACGCCAGCCTGGCTTCTTCTCCTCAGTGACCTTC
TGTCCCTGGTGGACCGGGGCTTTGTCTTACGCTGGTCCGGGCCACTACAAG
CAGGTAGGAGTGGCGTGGCCAGGTTGGCATGGCATGGATGGAAGCGCGA
GC

FIG. 6A (4 of 7)

Exon 103340 to 103590

CAATGTTGACATCACTGATGGCCACCCCCTCTCCTGCAGGTGGCCACGGGGT
CCAGTCGTCCCCTAATCCAGCAGCCCTGCTGACCCCTGCGCATGGAATTCACCGG
CATCCTGTGCAGCCACGAGCACTACGTGACCCCTCAACCTCCCCTGCTGCCCC
TGTCACCTCCAGCCTCGCCCTCCCCTCTGTGTCTCCACCACCTCCCAAGTG
GGCTGCCTTCACTTCTGCTCCTCTTTGACCTACAA

Exon 103990 to 104220

TGACCCITGACCGTGGCATCCCCATTTTTCCCCCACTCTGCAGAGCTCCAC
CTTCTCCAGCCAAGCCCCGACCCCAAGGTGACCAGCATGTTCGAACTGAGT
GGACCATTCCGGCAGCAGCACTTCCTAGCTGGGCTCCTGCTGACGGAGCCGG
CACTGGCCCTCGAACCTGAGGCTGAAGGTGAGCAGAGCTCTGTCTAGCCCC
AGGACAGGTGGGACAGTCCAG

Exon 104220 to 104480

GGAGCCATGTCCACCCTGTCTCAGCACCTATTACCCCATAGGGCATTCCTG
TTGCACAAGAGGCCCATCAGTGCTGTGCACAGCCTGCTATGTGGCCATGACA
CTGACCCCGCTACGCCCGAGGCCACTGTGAAGGCTCCTGTGGCCGAGCTGTA
CTGCCCACTGCTATCGATTSCACGGGATACCTGCCACGGCTGCATGACTTTG
CTGCTCAGTGGCCAGGGGAAGATGGGGTCACATGATCCAGGGACTTGGTC

Exon 108850 to 109100

ACCAAGGGTTTATCTTTCTTTCCCTCTGTCTTTCCCTGCCAGAGGGCCAGGTC
AGCGGTCAAGACTGGCCCTCAATGCTTGACTCAGACACAGAAGGCGAAGGGG
ACATTCCGGGTACCATCAACCCCTCTGTGGCCATGGCCATTGCTGGTGGCCCCC
TAGCCCCCTGGCTCCCGGGCCAGCATCTCCCAGGGGCCACCAACGGTGAGTA
GGGAGGCTTGTCCTCCATAGACATCATCCACTTTGAATGAGA

Exon 109140 to 109410

TCACATGGAGAAATGAAATTGACTTTGATTCTCTCTGCCCCAGGCCTCT
CGCGCAGGCTGTGCCCTCTCTGCTGAGTCAAGCCGGACCTTGCTGGCGTGTGT
GCTGTGGGTGCTGAAAAACACCGAGCGGGCGCTCTCGACGCTGGGGCACT
GACCTGACACTCCCCAGCTGGGACGTCTGTTGGATTGTGTACCTTTGCCT
AGCTGCCTTTGAGTACAAGGTTTGAAGGGCTGGGCAGGAGATGATGGAGGGG
GCAGGCTA

Exon 110310 to 110530

GAAAGAGCAGAGTCAGCCTGGAAACCCAGTTCTCTGCACCCCAGGGGAA
AAAGGCCTTTGAACGCATCAACAGCCTCACATTCAAAAAATCTCTGGATATG
AAGCGCGGCTAGAGGAGCCATTCTGGGTACCATCGAGCTCGACAAGAA
ATGGTTCGGCGAAGTCGTGGTAAGAGGGTGACATACCCACGTGTCCCCATCC
CACCAGCTGCTCCCA

Exon 110770 to 110940

TGTGTTTTTACGCATCTGTGATCGTGACCCACGCTCTCAGAGAGGAGCCG
TTTGGGAATCCGGAGAAATGCGCTGGCGGAAGAGCGTCACACACTGGAAGC
AAACCTCAGACCGGTGGACAAGTAGGTGTGGCAGGAGGGTGTCTGCTGAG
TTCAGAACAGTTTG

Exon 111590 to 111770

ATCTCACCCCGAGTGGGCCCCCAAGACCTCCTTTCCTTCCAGGACCAAGG
ATGAAATGGAACACGAGGCCTTGGTGAAGGGAACCTGGCAACCGAGGCAA
GCCTAGTGGTTCTCGACACACTGGAGATCATCGTGCAGGTAGGGCTTGATCC
AGCATCTGCCTTGTGCTCTGAGCCCA

Exon 111830 to 112050

ACCCTAGGCTCTAACACCTGGATTCTTGACCCCTTCCCTCCAGACGGTGATG
CTTTCAGAGCCCGGAGAGCGTCTTGGGGGCGAGTCTGAAGGTTGTGCTGT
ACAGCCTGGGCGAGTGGCCAGAGTGCCCTCTTCTTGACGATGGCTGGCCAC
CCAGAGGGCCCTTGTGTCCAAGGTGAGCACCCTCAACAACCATGATTCTTA
GAAAAACAGTAG

Exon 112910 to 113140

AACGGGGAGGGGCTGGACAGTGTCTGTCTGGTCCCTTGGGGGCGATCCCGG
AGCTGCTGTTTCGAGGAGGACACGAGCTGTGTGCCGACCTGTGCCTGAGGCT
CCTACGACACTGTGGCAGCCGCATCAGCACCATCCGACGACGCGACGCGCC
TGCTGTACCTGTCTATGCGACAGAACTTCGAGATCGGCCACGTGAGTGGG
GCTAGGAGGCATGGTCCACACATGGCTCTGGTC

Exon 114090 to 114340

TCTGAGACTCCCGGCTCCACCTCCCGCCCTGTCCCTGCAGAACTTTGCCCG
TGTGAAGATGCAGGTACCATGTCTCTCTCGTCCCTGGTGGGAGCAGCGAG
AACTTCAGTGAAGGACCTGCGACGTTCACTCAAAACCATCTCACTATG
CTGAGGAGGACATGGGCTGCGGGACAGCACCCTCGCAGACGAGGTGACAC
CTGCTGGGTCCCGCCCGGCTCCCTTCATATAACTCCCAAC

FIG. 6A (6 of 7)

Exon 114370 to 114550

ATGCTCTCATTTGGCCCTGGACGTTCCCGGCTCCAGGTCAGGACCTGATGT
TCAACCTGCACATGATCCTGACGGACCGGTGAAGATGAAGGAACACCGG
AGGACCTGAGATGCTCATCGACCTCATGTACAGGTGAGGTGGGCCAGCTGG
CACCTTCAGCCACGCCACGCCCA

Exon 116900 to 117170

AGGTGAGTCCCTCCTCACATCCCCCTCACCTGGACTCCAGAATTGCGCGGG
GCTACACAGGGCTACCGGACCTTCGGGTGACCTGGTTCCAGAACATGGCCGG
GAAGCACCGGACCTGGGCAACACGCCAGGCGGCCAGTGCATGGTCCA
CGCGCCCGCCCTCGTGGCTGAGTACCTCGCCCTGCTCGAGGACAGCGCCAC
CTGCCCCGTGGCTGCGATTTCCTTCAGGTGAGTGCCAGGGTTGCCAGGT
GGCGGACGGCA

Exon 117170 to 117410

ACGAGTGCAGTGGGGACAGGGTCTGACGCCACCTTCCCCACCCAGAACAT
CTCATCCAACGTGCTAGAGGAGTCCGCCATCTCCGACGACATCCTGTGCCCC
GACGAGGAGGGCTTCTGCTCCGGGAAGCACTTCACTGAGCTGGGGCTGGTAG
GCTTCTTGGACAGGCGAGCGGCTACTTCACCATGGTGAGGCTTGGGGACT
GGTGCGAGGAGGGGCTCGGGCCAGGGAGGT

Exon 121670 to 121900

GAGAGGAAGACAGTTTGGGGAATCCTGACCCCACTCACCTCAGGGCGGGC
TCTACGAGGCGGTGAATGAGGTCTACAAGAACCTCATCCCCATCCTGGAAGC
CCACCGTGACTACAAGAAGCTGGCCGCGGTGCACGGCAAACTGCAGGAGGC
CTTCACAAAGATCATGCACCAAGTGGGCCAGGACCCCCCTCCCCAGACCCA
CCCCAGCCCCACTCCTCATCC

Exon 121910 to 122000

CCCCAGGGATCTGCTGACCTTGACCTTCTCTTCCCCACAGAGTTCCGGCTGG
GAGGTGAGTCAGCCTTGGTGGACAGCCACCTGCCCTCG

Exon 123290 to 123510

TCCAGCAGGGGCTCCCCGGACAACACACCTTTCTCACAGCCCCAGCGGT
GTTCGGGACGTATTTCGCGGTGGGCTTCTACGGCGCCACTTCGGTGACCTGG
ATGAGCAGGAGTTTGTTGTAACAAGGAGCCATCGATCAGGAAGCTGGCAGAGAT
CTCACACCGGCTGGAGGCATGTCTTGTGGTTGGGGTGGAACGGGGCATGG
GGTGCTCTGGG

Exon 123510 to 123633 (end clone)

GGCTGGAGTAGGGGCTGTCCCTGGTGGCCCGGAGTCAGCCCTGTGTCTCCA
GGAGTTCTACCGGAGAGATTGGCGACGACGTCTGAGATTATCAAAGAC
TCTAACCTGTGGACAGTC

FIG. 6B


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hCLASP4      FKS HLESTIYTDQLHVHKFFHHQC LIQS-----GSKVEPGELIKYKLCLHMA 794
hCLASP5      IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHKLKSIICLNS 715
hCLASP3      VEVVAVSSVHTQDPYLDKRFALVNALDEH-LFFVRIQDMRIMENNLKSSISALNS 780
hCLASP7      ISTHLVSTVYTDQHLHNFQKQKTRB-----GAQALGNELVRLKSLHMA 787
hCLASP7      VELTAVSSVHTQDPYLDKRFITLVHVEEG-AFFFLKDTVLSEGNVQELERSLAALRLA 767
hCLASP1      VSTFVSVTNTQDPHVNAFFQCCKREKQ-----MSQSPTSNFIRSCKNLLNVE 887
..      *::..* :.:..* * : : :
..      *::..* :.:..* * : : :

hCLASP4      EIDVMIOFLPVLILQLEF-----VLNTMTH-----EDDVP 824
hCLASP5      RLEPLVLFLHLVLDKLEFQLSVQPMVIAGQTANFSQAFESVVAIANSLHNSKDLSDQH 775
hCLASP3      QLEPVRFLHLLLDKLELVLIRPPVIAGQIVNLQGSFEAMASINIRLHNLEGNHDQH 840
hCLASP2      EGVVMAIFLPTILNQLEF-----VLT-RAT-----QEEVA 816
hCLASP7      SPEPLVAFSHHVLDKLELVLIRPPIISQIVNLGRGAFEMAHVSVLVRHSLEAQDARG 827
hCLASP1      KIHAMSFLPILNQLEF-----VLVQNE-----EDEIT 916
..      *::..* :.:..* * : : :

hCLASP4      INCTMV-LLHIVSKCHEEGLDS-----YLRSFIKYS-----FRPEKP 860
hCLASP5      RNCILASYVHVYFRLPEVQRDVPKSGAPTALLDPRS YHTYGR TSAA VSSKLLQARVMSS 835
hCLASP3      RNSLLASYIHVYFRLPNTYFNSSSPG-PGGLGGSVHYATMARSAVPA S LNNRSLN 899
hCLASP2      VNMTRV-IHHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY 852
hCLASP7      HQPLQAVYHYAFRLPGTEPSLPDGAPP---VTQVAATLARGSGRPASLYLARSKSIS 883
hCLASP1      TTVTRV-LPDIIVAKCHEEQLDH-----SVQSYIKFV-----FKTRAC 952
..      *::..* :.:..* * : : :

hCLASP4      SAPOQOLIH-----ETLATTMIAILKQS-----863
hCLASP5      SNPDLAGTHSADEEVKNIMSSKIADRNCRMSYSCSGSDAPSSPA-----882
hCLASP3      SNPDISGTPSPDDEVRSIIGSKGLDRSNWVNTGGPKAAPWGSNFPSPAESTQAMDRSC 959
hCLASP2      VASEYKTVH-----EELTKSMTIILKPS-----875
hCLASP7      SNPDLA VAPGSVDDEVSRILASKLLHEELA-LQ-----915
hCLASP1      KE---RPVH-----EDLAKNVTGLLKN-----972
..      *::..* :.:..* * : : :

hCLASP4      -----ADFLSINKLLKYS-----WFFFI IAKSM 907
hCLASP5      -----APRPASKKHFEELALQ-----MVVSTGMVKSM 910
hCLASP3      NRMSSHETETSSFLQTLTGRLP TKKLFHEELALQWVVCSGSVRESALQQAWFFPELMVKSM 1019
hCLASP2      -----ADFLTSNKLLKYS-----WFFFDVLKSM 899
hCLASP7      -----WVSSSAVREALQHA-----WFFFQLMVKSM 942
hCLASP1      -----DSPTVKHVLKHS-----WFFFAILLKSM 995
..      *::..* :.:..* * : : :

Cadherin Cleavage
hCLASP4      ATYLLENKIKLEKRGFPETYHHVLHSLLLAIIPHVTIRYAEIPDE---SRNVNVLAS 964
hCLASP5      AQHVHNDKRDSESRRTFSDREMDDIITIVNVVTSEIAALLVKPKENEQAEMNLSLAF 970
hCLASP3      VHHLYFNDKLEAKRSEFPERFMDIDIAALVSTIASDIVSRFQKDTM---VERLNTSLAF 1076
hCLASP2      AQHLIENSKVKILRNQRFPSASYHHAETVNNMLMPHITQKFGMDPEA---SKNANSLAV 956
hCLASP7      ALHLLLGRLDTRKLEFPGRLDDITALVGSVGLVITRVHKDVEL---AEHLNLSLAV 999
hCLASP1      AQHLIDNKKIQLRPPQRFPSYQNELDNLVMLVSDHVINKYKDALEE---TRATNSVAR 1052
..      *::..* :.:..* * : : :

hCLASP4      FLKRCLTLMDRGFTFNLINDYISGFSFKDP-----SLVAEYKFDFLQTCNHEHYIPLNL 1019
hCLASP5      FLYDLLSLMDRGFVFNLRHYCSQLSAKLSNL---FLVLSMRELFRLILCSHEHYIANL 1027
hCLASP3      FLNDLLSVMDRGFVFLSLIKSCYQVSSKLSLNPFSLVLSALDFLRILCSHEHYVTIAN 1136
hCLASP2      FIKRCFTFMDRGFVFKQINNYISCFAPGDP-----RLVYKFDFLRVLCNHEHYIPLNL 1011
hCLASP7      FLSDLLSLVDRGFVFLVRAHYKQVATRLQSSNPNAALLTLRMEFTRLILCSHEHYIPLNL 1059
hCLASP1      FLKRCFTFMDRGFVFKMNVNYSMFSSGDL-----RLVYKFDFLQTCNHEHYIPLNL 1107
..      *::..* :.:..* * : : :

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FIG. 7 (3 of 6)

hCLASP4 ERFGTENVKIIQDSKVNAKELDPKTAHIOHIVVKKHFDOKELTERKTEFERNNHNISRFV 1799
 hCLASP5 QQFGAEFVEVVKDSIPVDKTKLDDNKAYIQHFFVEHYFDEYEMKDRVTYFEKNFNLRRFM 1810
 hCLASP3 ERFGSEVDVVEIKDSNPNVDKCKLDDNKAYIQHFFVEHYFDEYEMKDRVTYFEKNFNLRRFM 1932
 hCLASP2 DRFGSEVDVVEIKDSNPNVDKCKLDDNKAYIQHFFVEHYFDEYEMKDRVTYFEKNFNLRRFM 1770
 hCLASP7 ERFGSEVDVVEIKDSNPNVDKCKLDDNKAYIQHFFVEHYFDEYEMKDRVTYFEKNFNLRRFM 1851
 hCLASP1 DRFGADNVKIIQDSKVNPNKDLDDNKAYIQHFFVEHYFDEYEMKDRVTYFEKNFNLRRFM 1972
 : * * : : : * * : : * * : * * : * * : * : : * :
 ITAM ITAM
 hCLASP4 FEAPYTLGKKKGCIIEQCKRRRTILTTNSFFVVKRIPINCEQQINLEKPIDGATDEIKD 1859
 hCLASP5 YTTPTTLGPRRGELHEQYRRNTVLTTHMAFFYIKTRISVIQKEEFVLTPIEVAIEDMKK 1870
 hCLASP3 YCTPTTLGDRAGHELHEQFKRRRTILTTSHAFYIKTRISVNIQKEEFVLTPIEVAIEDMQK 1992
 hCLASP2 FEMPTQTGKRGGVEEQCKRRRTILTTAHCFYVVKRIPVMYQHHTILNPIEVAIDEMSK 1830
 hCLASP7 FCTPTTLDGRAGHELHEQHKRRRTILTTDHAFYIKTRIRVCHREETVLTPIEVAIEDMQK 1911
 hCLASP1 FETPTTLGKKHGGVAEQCKRRRTILTTSHLFYVVKRIRIQVISQSSTELNPIEVAIDEMSR 2032
 : * * : : : * * : : * * : * * : * * : * : : * :
 Coiled-coil
 hCLASP4 KTAELQKLCSSSTDVDMQLQKLGQSVSVQVNAAGPLAYARAFNLDSQASKYPPKKVSELK 1919
 hCLASP5 KTLQLAVAINQEPDDAKMLQMVLOGSVGATVNOGPLEVAQVFLAEIPADPKLYRHHNKLK 1930
 hCLASP3 KQELAFATHQDPADPKMLQMVLOGSVGTTVNOGPLEVAQVFLAEIPADPKLYRHHNKLK 2052
 hCLASP2 KVAELRQLCSSAEVDIMKILQKLGQSVSVQVNAAGPLAYARAFNLDDTNKRYPDNKVKLLK 1890
 hCLASP7 KTRLELAFATEQDPDDAKMLQMVLOGSVGPTVNOGPLEVAQVFLAEIPADPKLYRHHNKLK 1971
 hCLASP1 KVSELNLCTKEEVDMSLQKLGQSVSVKVNAGPMAYARAFLEETNAKYPDNQVKLLK 2092
 * . * * * * : : * * : * * : * * : * * : * : : * :
 Coiled-coil
 hCLASP4 DMFRKFIQACSIALELNERLIKEDOVEYHEGLKSNFRDMVKELSDIHEQILQEDTMHSP 1979
 hCLASP5 LCFKFIPIMRGCEAVEKNKRLITADREYQCELKKNYNKLKENLRPMERKIPELYKPIFR 1990
 hCLASP3 LCFKDFTKRCCEALRKNNKSLIGPVQKEYQRELGLKSSP----- 2090
 hCLASP2 EVFRQFVEACGCEALAVNERLIKEDOLEYQEBMKANYREMAKELSEIMHEQICPLEEKTSS 1949
 hCLASP7 LCFKDFCKKCEALRKNNKSLIGPVQKEYYHRELERNYCLREALQPIILTORLPQLMAPTPO 2030
 hCLASP1 EIFRQFADACGCEALVNERLIKEDOLEYQEBELRSHYKMDLSELSTVMNEQITGRDDLKSR 2152
 * . * * : : * * : * * : * * : * * : * : : * :
 PDZ ligand
 hCLASP4 WMSNTLHVFCALISGTSSDRGYGSPRAEV----- 2008
 hCLASP5 VESQKRDSFHRSSFRKCEITQLSQGS----- 2015
 hCLASP3 ----- 2015
 hCLASP2 VLPNSLHI FNAISGTPSTSMVHGMTSSSEVV----- 1980
 hCLASP7 --PGLRNSLNRAFRKADL----- 2047
 hCLASP1 GVDQCTRVISKATPALPTVSISSAEV----- 2180

FIG. 7 (6 of 6)